

# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/554,068  
Source: IFWO  
Date Processed by STIC: 10/2/06

# *ENTERED*

## **CRF Errors Edited by the STIC Systems Branch**

Serial Number: 10/554,068

CRF Edit Date: 10/2/06  
Edited by: M2

Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

---

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

---

Deleted: \_\_\_ invalid beginning/end-of-file text ; \_\_\_ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

---

Moved responses to same line as heading/numeric identifier, specifically:

---

Other: Sequence 28 - corrected the spelling of "position"

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IFWO

## **RAW SEQUENCE LISTING**

PATENT APPLICATION: US/10/554,068

DATE: 10/02/2006

TIME: 11:30:02

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10022006\J554068.raw

3 <110> APPLICANT: Kadler, Karl  
4 Bulleid, Neil  
5 Ashcroft, Gillian  
7 <120> TITLE OF INVENTION: Modified Peptides and Their Uses  
9 <130> FILE REFERENCE: 17695-0002  
11 <140> CURRENT APPLICATION NUMBER: US 10/554,068  
12 <141> CURRENT FILING DATE: 2005-10-21  
14 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/00171  
15 <151> PRIOR FILING DATE: 2004-04-21  
17 <150> PRIOR APPLICATION NUMBER: GB 0309064.4  
18 <151> PRIOR FILING DATE: 2003-04-22  
20 <160> NUMBER OF SEQ ID NOS: 28  
22 <170> SOFTWARE: PatentIn version 3.3  
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26 <212> TYPE: DNA  
27 <213> ORGANISM: Artificial Sequence  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: Oligonucleotide for PCR  
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36 <210> SEQ ID NO: 2  
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38 <212> TYPE: DNA  
39 <213> ORGANISM: Artificial Sequence  
41 <220> FEATURE:  
42 <223> OTHER INFORMATION: Oligonucleotide for PCR  
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54 <223> OTHER INFORMATION: Oligonucleotide for PCR  
56 <400> SEQUENCE: 3  
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62 <212> TYPE: DNA  
63 <213> ORGANISM: Artificial Sequence  
65 <220> FEATURE:  
66 <223> OTHER INFORMATION: Oligonucleotide for PCR

RAW SEQUENCE LISTING  
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Input Set : N:\AMC\PTO.AMC.txt  
Output Set: N:\CRF4\10022006\J554068.raw

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77 <220> FEATURE:
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122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: DNA molecule based on procollagen type III N-propeptide.
127 Sequence prior to N100 replaced with the sequence for the G123
128 domains of the alpha3 chain of laminin-5 whilst retaining the
129 collagen III signal sequence.
131 <400> SEQUENCE: 9
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136 actgagaata tgtttgtat gtaccttggaa aataaagatg cttcccgggaa ctacatcgcc 180
138 atggcagttt tggatggcca gtcacactgt gtctacaacc tgggggaccg tgaggctgaa 240
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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/554,068

DATE: 10/02/2006  
TIME: 11:30:02

Input Set : N:\AMC\PTO.AMC.txt  
Output Set: N:\CRF4\10022006\J554068.raw

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148	agtgcactaa	gttccctcc	atacaaagg	tgtattgaat	tagatgacct	caatgaaaat	540
150	gttctgagct	tgtacaactt	caaaaaaaaca	ttcaatctca	acacaactga	agtggagcct	600
152	tgtagaagga	ggaagaaga	gtcagacaaa	aattatttt	aaggtacggg	ctatgctcg	660
154	gttccaactc	aaccacatgc	teccatecca	accttggac	agacaattca	gaccaccgtg	720
156	gatagaggct	tgctttctt	tgcaaaaaac	ggggatcgct	tcatatctct	aatatagaa	780
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160	ggagacgcca	taaacaaacgg	cagagaccat	tcgattcaga	tcaaaattgg	aaaactccaa	900
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164	ttcagcacat	attatctggg	aggaattcca	attgcaatca	gggaaagatt	taacatttct	1020
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176	gatagcggcg	gcccaatttt	taaatctca	cagacgtata	tggatggtt	actgcattat	1380
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236	caaggagaaaa	gtggtcgacc	aggtcctct	gggcacatcg	gtccccggagg	tcagcctgg	3180
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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/554,068

DATE: 10/02/2006  
TIME: 11:30:02

Input Set : N:\AMC\PTO.AMC.txt  
Output Set: N:\CRF4\10022006\J554068.raw

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308	tactgggttg	acccttaacca	aggatgcaaa	ttggatgct	tcaaggatatt	ctgtaatatg	5340
310	gaaactgggg	aaacatgcat	aagtgc	ccttgaatg	ttccacggaa	acactgg	5400
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322	tgcacgaaac	acactgggg	atggagcaaa	acagtctt	aatatcgac	acgcaaggct	5760
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330	<211>	LENGTH:	1950				
331	<212>	TYPE:	PRT				
332	<213>	ORGANISM:	Artificial Sequence				
334	<220>	FEATURE:					

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/554,068

DATE: 10/02/2006  
TIME: 11:30:02

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Output Set: N:\CRF4\10022006\J554068.raw

335 <223> OTHER INFORMATION: Sequence of the modified pro-alpha chain  
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 344 20 25 30  
 347 Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr  
 348 35 40 45  
 351 Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val  
 352 50 55 60  
 355 Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu  
 356 65 70 75 80  
 359 Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val  
 360 85 90 95  
 363 Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn  
 364 100 105 110  
 367 Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr  
 368 115 120 125  
 371 Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu  
 372 130 135 140  
 375 Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro  
 376 145 150 155 160  
 379 Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp  
 380 165 170 175  
 383 Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn  
 384 180 185 190  
 387 Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser  
 388 195 200 205  
 391 Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln  
 392 210 215 220  
 395 Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val  
 396 225 230 235 240  
 399 Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser  
 400 245 250 255  
 403 Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser  
 404 260 265 270  
 407 Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg  
 408 275 280 285  
 411 Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp  
 412 290 295 300  
 415 Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp  
 416 305 310 315 320  
 419 Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg  
 420 325 330 335  
 423 Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys  
 424 340 345 350  
 427 Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys  
 428 355 360 365  
 431 Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 10/02/2006  
PATENT APPLICATION: US/10/554,068                    TIME: 11:30:03

*FYI*  
Input Set : N:\AMC\PTO.AMC.txt  
Output Set: N:\CRF4\10022006\J554068.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:28; Xaa Pos. 2,3,5,7,8,10,11

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/554,068

DATE: 10/02/2006

TIME: 11:30:03

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10022006\J554068.raw

L:2217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0

## **Raw Sequence Listing before editing (for reference only)**



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/554,068**

**DATE: 09/29/2006**  
**TIME: 10:16:06**

**Input Set : F:\17695-0002.txt**  
**Output Set: N:\CRF4\09292006\J554068.raw**

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3 <110> APPLICANT: Kadler, Karl
4       Bulleid, Neil
5       Ashcroft, Gillian
7 <120> TITLE OF INVENTION: Modified Peptides and Their Uses
9 <130> FILE REFERENCE: 17695-0002
11 <140> CURRENT APPLICATION NUMBER: US 10/554,068
12 <141> CURRENT FILING DATE: 2005-10-21
14 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/00171
15 <151> PRIOR FILING DATE: 2004-04-21
17 <150> PRIOR APPLICATION NUMBER: GB 0309064.4
18 <151> PRIOR FILING DATE: 2003-04-22
20 <160> NUMBER OF SEQ ID NOS: 28
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
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56 <400> SEQUENCE: 3
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*sls  
P.8*  
*Does Not Comply  
Corrected Diskette Needed*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/554,068

DATE: 09/29/2006

TIME: 10:16:06

Input Set : F:\17695-0002.txt

Output Set: N:\CRF4\09292006\J554068.raw

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 96 <210> SEQ ID NO: 7  
 97 <211> LENGTH: 32  
 98 <212> TYPE: DNA  
 99 <213> ORGANISM: Artificial Sequence  
 101 <220> FEATURE:  
 102 <223> OTHER INFORMATION: Oligonucleotide for PCR  
 104 <400> SEQUENCE: 7  
 105 gtgttaaaaac ggcggccgt gaattgtaat ac 32  
 108 <210> SEQ ID NO: 8  
 109 <211> LENGTH: 32  
 110 <212> TYPE: DNA  
 111 <213> ORGANISM: Artificial Sequence  
 113 <220> FEATURE:  
 114 <223> OTHER INFORMATION: Oligonucleotide for PCR  
 116 <400> SEQUENCE: 8  
 117 gtattacaat tcagcggccg ccgttttaca ac 32  
 120 <210> SEQ ID NO: 9  
 121 <211> LENGTH: 5853  
 122 <212> TYPE: DNA  
 123 <213> ORGANISM: Artificial Sequence  
 125 <220> FEATURE:  
 126 <223> OTHER INFORMATION: DNA molecule based on procollagen type III N-propeptide.  
 127 Sequence prior to N100 replaced with the sequence for the G123  
 128 domains of the alpha3 chain of laminin-5 whilst retaining the  
 129 collagen III signal sequence.  
 131 <400> SEQUENCE: 9  
 132 atgatgagct ttgtcaaaa ggggagctgg ctacttctcg ctctgcttca tcccactatt 60  
 134 atttggcaa catctctgtc ttgtttctc caaaggccca actcaagaga aaatgggggt 120  
 136 actgagaata tgtttgtat gtaccttggaa aataaaatgt cctcccgaa ctacatcgcc 180  
 138 atggcagttt tggatggcca gtcacacgt gtctacaacc tgggggaccg tgaggctgaa 240  
 140 ctccaaagtgg accagatctt gaccaagagt gagactaagg aggtagttt ggatcggttg 300

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/554,068**

**DATE: 09/29/2006**  
**TIME: 10:16:06**

**Input Set : F:\17695-0002.txt**  
**Output Set: N:\CRF4\09292006\J554068.raw**

142	aaatttcaga	gaatttatca	gtttgcaagg	cttaattaca	ccaaaggagc	cacatccagt	360
144	aaaccagaaa	cacccggagt	ctatgacatg	gatgtagaa	atagcaatac	actccttaat	420
146	ttggatcctg	aaaatgttgt	attttatgtt	ggaggttacc	cacctgattt	taaacttccc	480
148	agtgcactaa	gttccctcc	atacaaaggt	tgtattgaat	tagatgacct	caatgaaaat	540
150	gttctgagct	tgtacaactt	caaaaaaaaca	ttcaatctca	acacaactga	agtggagcct	600
152	tgtagaagga	ggaaggaaga	gtcagacaaa	aattattttg	aaggtacggg	ctatgctcg	660
154	gttccaactc	aaccacatgc	tcccatccca	accttggac	agacaattca	gaccaccgtg	720
156	gatagaggct	tgctttctt	tgcagaaaac	ggggatcgct	tcatatctct	aatatagaa	780
158	gatggcaagg	tcatggtgag	atacaaactg	aattcagacg	taccaaaga	gagaggagtt	840
160	ggagacgcca	taaacaacgg	cagagaccat	tcgattcaga	tcaaaaattgg	aaaactccaa	900
162	aagcgtatgt	ggataaatgt	ggacgttcaa	aacactataa	ttgatggtga	agtatttgat	960
164	ttcagcacat	attatctggg	aggaattcca	attgcaatca	gggaaagatt	taacatttct	1020
166	acgcctgctt	tccgaggctg	cataaaaat	ttgaagaaaa	ccagtggtgt	cgttagattg	1080
168	aatgatactg	tggagtaac	caaaaagtgc	tcggaagact	ggaagctgt	gcgatctgcc	1140
170	tcattctcca	gaggaggaca	attgagttc	actgatttg	gcttaccacc	tactgaccac	1200
172	ctccaggcct	catttggatt	ttagacctt	caaccagtg	gcatattatt	agatcatcag	1260
174	acatggacaa	ggaacctgca	ggtcactctg	gaagatggtt	acattgaatt	gagaccacgc	1320
176	gatagcggcg	gcccaatttt	taaatactcca	cagacgtata	tggatggttt	actgcattat	1380
178	gtatctgtaa	taagcgacaa	ctctggacta	cggcttctca	tcgatgacca	gcttctgaga	1440
180	aatagcaaaa	ggctaaaaca	catttcaagt	tcccggcagt	ctctgcgtct	gggcgggagc	1500
182	aattttgagg	gtttagtttag	caatgtttt	gtccagaggt	tatcactgag	tcctgaagtc	1560
184	ctagatttga	ccagtaactc	tctcaagaga	gatgtgtccc	tgggaggctg	cagtttaaac	1620
186	aaaccacctt	ttctaattgtt	gcttaaaggt	tctaccaggt	ttaacaagac	caagactttt	1680
188	cgtatcaacc	agctttgca	ggacacacca	gtggcctccc	caaggagcgt	gaaggtgtgg	1740
190	caagatgcta	atggtcaagg	acctaaggc	cccaaggggag	atccaggccc	tcctggatt	1800
192	cctgggagaa	atggtgaccc	ttgtattcga	ggacaaccag	ggccccctgg	ttctcctggc	1860
194	ccccctggaa	tctgtatc	atgcctact	ggtcctcaga	actattctcc	ccagtatgt	1920
196	tcatatgatg	tcaagtctgg	atgagcgt	ggaggactcg	caggctatcc	tggaccagct	1980
198	ggccccccca	gccctcccg	tcccccgtt	acatctggtc	atcctggttc	ccctggatct	2040
200	ccaggatacc	aaggacccccc	ttgtgaacct	ggcaagctg	gtccttcagg	ccctccagga	2100
202	cctcctggtg	ctataaggc	atctggctt	gctgaaaag	atggagaatc	agtagaccc	2160
204	ggacgacctg	gagagcgagg	attgcctgga	cctccaggta	tcaaaggctc	agctggata	2220
206	cctggattcc	ctggatgaa	aggacacaga	ggcttcgatg	gacgaaatgg	agaaaagggt	2280
208	gaaacagggtg	ctcctggatt	aaagggtgaa	aatggcttc	caggcgaaaa	tggagctcct	2340
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212	gcaggtgctc	ggggtaatga	cggtgctcg	ggcagtgtat	gtcaaccagg	ccctcctgg	2460
214	cctcctggaa	ctggcggatt	ccctggatcc	cctggtgcta	agggtgaagt	tggacctgca	2520
216	gggtctcctg	gttcaatgg	tgccccctg	caaagaggag	aacctggacc	tcagggacac	2580
218	gctggtgctc	aaggctctcc	ttggccctct	gggattaatg	gtagtcctgg	tgttaaaggc	2640
220	gaaatgggtc	ccgctggcat	tcctggagct	cctggactga	tgggagcccc	gggtcctcca	2700
222	ggaccagccg	gtgctaatgg	tgctcctg	ctgcgagggt	gtgcagggt	gcctggtaag	2760
224	aatggtgcca	aaggagagcc	cgaccacgt	ggtgaacgcg	gtgaggctgg	tattccaggt	2820
226	gttccaggag	ctaaaggcga	agatggcaag	gatggatcac	ctggagaacc	tggtgcaaat	2880
228	ggccttccag	gagctgcagg	agaaagggtt	gccccctgg	tccgaggacc	tgctggacca	2940
230	aatggcatcc	caggaaaaaa	gggtcctgt	ggagacgtg	gtgcctcagg	ccctgcaggg	3000
232	cccaaggagag	ctgctggaga	acctggcaga	gatggcgtcc	ctggaggctc	aggaatgagg	3060
234	ggcatgcccc	gaagtccagg	aggaccagga	agtgtatgg	aaccaggccc	tcccgaaagt	3120
236	caaggagaaa	gtggtcgacc	aggtcctct	gggcattctg	gtccccggagg	tcagcctgg	3180
238	gtcatggct	tcccccgtcc	taaaggaaat	gatggtgc	ctggtaagaa	tggagaacga	3240

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/554,068

DATE: 09/29/2006

TIME: 10:16:06

Input Set : F:\17695-0002.txt

Output Set: N:\CRF4\09292006\J554068.raw

240	ggtgccctg	gaggacctgg	ccctcagggt	cctcctggaa	agaatggta	aactggacct	3300
242	caaggacccc	cagggcctac	tgggcctgg	ggtgacaaag	gagacacagg	accggcctgg	3360
244	ccacaaggat	tacaaggctt	gcctggtaca	ggtggctc	caggagaaaa	tggaaaacct	3420
246	ggggAACCAg	gtccaaAGGG	tgatGCCG	gcacctggag	ctccaggagg	caagggtgat	3480
248	gctgggcc	ctggtaacg	tggacctct	ggattggcag	ggggccccagg	acttagaggt	3540
250	ggagctggtc	cccctggtcc	cgaaggagga	aagggtgctg	ctggcctcc	tggccacct	3600
252	ggtgctgctg	gtactcctgg	tctgcaagga	atgcctggag	aaagaggagg	tcttggaa	3660
254	cctggtccaa	agggtgacaa	gggtgaacca	ggcgccccag	gtgctgatgg	tgtcccagg	3720
256	aaagatggcc	caaggggtcc	tactggtc	attggctc	ctggcccagc	tggccagcct	3780
258	ggagataagg	gtgaaggtgg	tgcggccg	cttccaggt	tagctggacc	tcgtggtagc	3840
260	cctggtgaga	gaggtgaaac	tggccctcca	ggacctgctg	gtttccctgg	tgctcctgg	3900
262	cagaatgggt	aacctggtgg	taaaggagaa	agaggggctc	cgggtgagaa	aggtgaagga	3960
264	ggccctcc	gagttgcagg	accccccgt	gttctggac	ctgctggcc	tcctggtccc	4020
266	caaggtgtca	aaggtaacg	tggcagtct	ggtggac	gtgctgctgg	cttccctgg	4080
268	gtcgtggtc	ttcctggtcc	tcctggtagt	aatgttaacc	caggaccccc	aggccacgc	4140
270	ggttctcc	gcaaggatgg	gccccccaggt	cctgcggta	acactgg	tcctggcagc	4200
272	cctggagtgt	ctggacccaa	agggtgatgt	ggccaaaccag	gagagaaggg	atgcctgg	4260
274	gcccaggggc	caccaggagc	tccaggccca	cttggattg	ctgggatcac	tggagcacgg	4320
276	ggtcttgcag	gaccaccagg	catgccagg	cctaggggaa	gccctggccc	tcagggtgtc	4380
278	aagggtgaaa	gtggaaacc	aggagcta	ggtctcagtg	gagaacgtgg	tcccctgg	4440
280	ccccagggtc	ttcctggtct	ggctggta	gctggtaac	ctggaaagaga	tggaaaccct	4500
282	ggatcagatg	gtcttccagg	cggagatg	tctctgg	gcaagggtg	tcgtggtaa	4560
284	aatggctc	ctgggtcccc	tggcgtc	ggtcatcc	gcccacctgg	tcctgtcggt	4620
286	ccagctggaa	agagtggta	cagaggagaa	agtggcc	ctggccctgc	tgggtctccc	4680
288	ggtcctgctg	gttcccgagg	tgctcctgg	cctcaaggcc	cacgtggta	caaaggtaa	4740
290	acaggtgaac	gtggagctgc	tggcatcaa	ggacatcg	gattccctgg	taatccagg	4800
292	gccccaggtt	ctccaggccc	tgctggta	cagggtg	tcggcagtcc	aggacctgca	4860
294	ggccccagag	gacctgttgg	acccagtgg	cctctggca	aagatggaa	cagtggacat	4920
296	ccaggtccca	ttggaccacc	agggcctcg	ggtacacag	gtgaaagagg	atctgagg	4980
298	tccccaggcc	acccaggc	accaggcc	cctggac	ctgggcccc	tggccttgc	5040
300	tgtgggtgt	ttggagccgc	tgccattgt	gggattgg	gtggaaa	tggcggttt	5100
302	gccccgtatt	atggagatg	accaatgg	ttcaaaatca	acaccgatg	gattatgact	5160
304	tcactca	ctgttaatgg	acaaatagaa	gcctcatta	gtcctgatgg	ttctcgtaaa	5220
306	aaccccgcta	gaaactgc	agacctgaaa	ttctgccatc	ctgaactcaa	gagtggagaa	5280
308	tactgggtt	acccta	aggatgaaa	ttggatg	tcaagg	tgtatcgat	5340
310	gaaactgggg	aaacatgcat	aagtgc	ccttgaatg	ttccacg	acactgg	5400
312	acagattcta	gtgctgagaa	gaaacacgtt	tggttgg	agtccatgg	tgggttt	5460
314	cagttagct	acggcaatcc	tgaacttc	gaagatgt	ttgatgt	gctggcattc	5520
316	cttcgacttc	tctccagcc	agcttccc	aacatcacat	atca	aatagcatt	5580
318	gcatacatgg	atcaggcc	tggaaatgt	aagaaggccc	tgaagctg	gggtcaat	5640
320	gaaggtgaat	tcaaggctg	aggaaatag	aaatccac	acacagt	ggaggatgg	5700
322	tgcacgaaac	acactgggg	atggagaaa	acagtctt	aatatcg	acgcaagg	5760
324	gtgagactac	ctattttaga	tattgcaccc	tatgacatt	gtggcctg	tcaagaattt	5820
326	ggtgtggacg	ttggccctgt	ttgcttttta	taa			5853
329	<210>	SEQ ID NO:	10				
330	<211>	LENGTH:	1950				
331	<212>	TYPE:	PRT				
332	<213>	ORGANISM:	Artificial Sequence				
334	<220>	FEATURE:					

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/554,068

DATE: 09/29/2006

TIME: 10:16:06

Input Set : F:\17695-0002.txt

Output Set: N:\CRF4\09292006\J554068.raw

335 <223> OTHER INFORMATION: Sequence of the modified pro-alpha chain  
 337 <400> SEQUENCE: 10  
 339 Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu  
 340 1               5               10               15  
 343 His Pro Thr Ile Ile Leu Ala Thr Ser Leu Ser Leu Phe Leu Gln Arg  
 344               20               25               30  
 347 Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr  
 348               35               40               45  
 351 Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val  
 352               50               55               60  
 355 Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu  
 356 65               70               75               80  
 359 Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val  
 360               85               90               95  
 363 Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn  
 364               100               105               110  
 367 Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr  
 368               115               120               125  
 371 Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu  
 372               130               135               140  
 375 Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro  
 376 145               150               155               160  
 379 Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp  
 380               165               170               175  
 383 Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn  
 384               180               185               190  
 387 Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser  
 388               195               200               205  
 391 Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln  
 392               210               215               220  
 395 Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val  
 396 225               230               235               240  
 399 Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser  
 400               245               250               255  
 403 Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser  
 404               260               265               270  
 407 Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg  
 408               275               280               285  
 411 Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp  
 412               290               295               300  
 415 Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp  
 416 305               310               315               320  
 419 Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg  
 420               325               330               335  
 423 Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys  
 424               340               345               350  
 427 Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys  
 428               355               360               365  
 431 Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 09/29/2006  
PATENT APPLICATION: US/10/554,068                    TIME: 10:16:07

Input Set : F:\17695-0002.txt  
Output Set: N:\CRF4\09292006\J554068.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:28; Xaa Pos. 2,3,5,7,8,10,11

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/554,068

DATE: 09/29/2006

TIME: 10:16:07

Input Set : F:\17695-0002.txt

Output Set: N:\CRF4\09292006\J554068.raw

L:2217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0

10/554,068

8

<210> 28  
<211> 11  
<212> PRT  
<213> Unknown

<220>  
<223> Sequence typically found in small leucine-rich proteoglycans.

<220>  
<221> MISC\_FEATURE *position*  
<222> (2)..(3)  
<223> X at *position* 2 or 3 may be any amino acid.

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> X at *position* 5 may be any amino acid.

<220>  
<221> MISC\_FEATURE  
<222> (7)..(8)  
<223> X at *position* 7 or 8 may be any amino acid.

<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)  
<223> X at *position* 10 may be any amino acid.

<220>  
<221> MISC\_FEATURE  
<222> (11)..(11)  
<223> X at *position* 11 is selected from L and I only.

<400> 28

Leu Xaa Xaa Leu Xaa Leu Xaa Xaa Asn Xaa Xaa  
1 5 10